



# SEQUENCE LISTING

<110> Commonwealth Scientific and Industrial Research Organization  
<120> Efficient gene silencing in plants using short dsRNA sequences  
<130> BCS-03-2001  
<150> US 60/447,711  
<151> 2003-02-19  
<160> 33  
<170> PatentIn version 3.3  
<210> 1  
<211> 341  
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<220>  
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<223> PolIII promoter region  
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<223> SalI restriction site  
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<223> poly T nucleotide stretch  
<220>  
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<222> (336)..(341)  
<223> XhoI restriction site  
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ctcgagatgt tgttggtacc agaaagtaaa taaatgttca atctctgatg ttctcaagta 60  
agtgaagtttt attgggaata atattaactc atgttcttct gcatttgatt ctttgccgc 120  
tctcttcttc tatcttaa atctgtgtatc tatttcacta ttgggctttt tattagtcta 180  
taatgggact caaaataagg ctttgccca catcaaaaag ataagtcaca aatcaaaact 240  
aaattcagag tcttttctcc cacatcggtc actgtactca ttttgtgttt gtttatatat 300  
tacacgaacc gatctttggt acgtcgactt ttttctcga g 341  
<210> 2  
<211> 429  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> sequence of the promoter of the 7SL-2 gene of Arabidopsis thaliana var. Landsberg erecta including 86 bases downstream of the transcription initiation site.

<220>  
 <221> misc\_feature  
 <222> (1)..(6)  
 <223> XhoI restriction site

<220>  
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 <222> (7)..(408)  
 <223> PolIII promoter region.

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 <222> (409)..(414)  
 <223> SalI restriction site

<220>  
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 <222> (415)..(423)  
 <223> poly T stretch

<220>  
 <221> misc\_feature  
 <222> (424)..(429)  
 <223> XhoI restriction site

<400> 2  
 ctcgagatgt tgttggtacc agaaagtaaa taaatgttca atctctgatg ttctcaagta 60  
 agtgagtttt attgggaata atattaactt atgttcttct tgcatttgat ttctttgccg 120  
 ctctcttctt ctatcttaaa tctgtgtata ctatttctact attgggcttt ttattagtct 180  
 ataatgggac tcaaaataag gctttggccc acatcaaaaa gataagtcac aaatcaaaac 240  
 taaattcaga gtcttttctc ccacatcggt cactgtactc ttttgtgttt gtttatatat 300  
 tacacgaacc gatctttggt acgtcgagct aagtaacatg agcttgtaac ccatgtgggg 360  
 acattaagat ggtggaacac tggctcgggt ccacgggccg gttctgttgt cgactttttt 420  
 tttctcgag 429

<210> 3  
 <211> 334  
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<220>  
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<220>  
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 <222> (1)..(6)  
 <223> EcoRI restriction site

<220>  
 <221> misc\_feature  
 <222> (7)..(313)

<223> Pol III promoter region

<220>

<221> misc\_feature

<222> (314)..(319)

<223> PvuI restriction site

<220>

<221> misc\_feature

<222> (320)..(328)

<223> poly T stretch

<220>

<221> misc\_feature

<222> (329)..(334)

<223> EcoRI restriction site

<400> 3

gaattcttat gcagcctgtg atggataact gaatcaaaca aatggcgtct gggtttaaga 60

agatctgttt tggctatgtt ggacgaaaca agtgaacttt taggatcaac ttcagtttat 120

atatggagct tatatcgagc aataagataa gtgggctttt tatgtaattt aatgggctat 180

cgtccataga ttcactaata cccatgccca gtacccatgt atgcgtttca tataagctcc 240

taatttctcc cacatcgctc aaatctaaac aaatcttggt gtatatataa cactgagggga 300

gcaacattgg tcacgatcgt ttttttttga attc 334

<210> 4

<211> 467

<212> DNA

<213> Artificial Sequence

<220>

<223> sequence of the promoter of the U3 snRNA gene of Arabidopsis thaliana var. Landsberg erecta including 136 bases downstream of the transcription initiation site.

<220>

<221> misc\_feature

<222> (1)..(6)

<223> EcoRI restriction site

<220>

<221> misc\_feature

<222> (7)..(446)

<223> Pol III promoter region

<220>

<221> misc\_feature

<222> (447)..(452)

<223> XhoI restriction site

<220>

<221> misc\_feature

<222> (453)..(461)

<223> poly T stretch

<220>

<221> misc\_feature

<222> (462)..(467)

<223> EcoRI restriction site

<400> 4

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gaattcttat gcagcctgtg atggataact gaatcaaaca aatggcgtct gggtttaaga      60
agatctgttt tggctatggt ggacgaaaca agtgaacttt taggatcaac ttcagtttat      120
atatggagct tataatcgagc aataagataa gtgggctttt tatgtaattt aatgggctat      180
cgtccataga ttcactaata cccatgccca gtacccatgt atgcgtttca tataagctcc      240
taatttctcc cacatcgctc aaatctaaac aaatcttggt gtatatataa cactgaggga      300
gcaacattgg tcacgacctt acttgaacag gatctgttct ataggctcgt acctctgttt      360
ccttgatttc tcaagagaca ggcccttaac cctggttgat gaaccatgac cgtgcggcta      420
gagcgtgatt gacggctacg atcgtcctcg agtttttttt tgaattc                    467

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<210> 5
<211> 456
<212> DNA
<213> Artificial Sequence

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<220>
<223> sequence of the promoter of the U6-26 snRNA gene of Arabidopsis
        thaliana var. Landsberg erecta including 3 bases downstream of
        the transcription initiation site, followed by a unique
        restriction site in front of an oligo dT stretch

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<220>
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<222> (1)..(6)
<223> XhoI restriction site

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<220>
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<222> (7)..(436)
<223> Pol III promoter region

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<220>
<221> misc_feature
<222> (437)..(442)
<223> SalI restriction site

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<220>
<221> misc_feature
<222> (443)..(450)
<223> poly T stretch

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<220>
<221> misc_feature
<222> (451)..(456)
<223> Sac I restriction site

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<400> 5
ctcgagcttc gttgaacaac ggaaactcga cttgccttcc gcacaatata tcatttcttc      60
ttagcttttt ttcttcttct tcgttcatac agtttttttt tgtttatcag cttacatttt      120
cttgaaccgt agctttcgtt ttcttctttt taactttcca ttcggagttt ttgtatcttg      180
tttcatagtt tgtcccagga ttagaatgat taggcacgca accttcaaga atttgattga      240
ataaaacatc ttattcttta agatatgaag ataatcttca aaaggcccct ggggaatctga      300
aagaagagaa gcaggcccat ttatatggga aagaacaata gtatttctta tataggccca      360
tttaagttga aaacaatctt caaaagtccc acatcgctta gataagaaaa cgaagctgag      420

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tttatataca gctagagtcg actttttttt gagctc

456

<210> 6  
<211> 488  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sequence of the promoter of the U6-26 snRNA gene of Arabidopsis thaliana var. Landsberg erecta including 20 bases downstream of the transcription initiation site, followed by a unique restriction site in front of an oligo dT stretch

<220>  
<221> misc\_feature  
<222> (1)..(6)  
<223> XhoI restriction site

<220>  
<221> misc\_feature  
<222> (7)..(468)  
<223> Pol III promoter region

<220>  
<221> misc\_feature  
<222> (469)..(474)  
<223> PvuI restriction site

<220>  
<221> misc\_feature  
<222> (475)..(482)  
<223> Poly T stretch

<220>  
<221> misc\_feature  
<222> (483)..(488)  
<223> XhoI restriction site

<400> 6  
ctcgagcttc gttgaacaac ggaaactcga cttgccttcc gcacaataca tcatttcttc 60  
ttagcttttt ttcttcttct tcgttcatac agtttttttt tgtttatcag cttacatttt 120  
cttgaaccgt agctttcgtt ttcttctttt taactttcca ttcggagttt ttgtatcttg 180  
tttcatagtt tgtcccagga ttagaatgat taggcacgca accttcaaga atttgattga 240  
ataaaacatc ttcattctta agatatgaag ataattctta aaaggcccct gggaatctga 300  
aagaagagaa gcaggcccat ttatatggga aagaacaata gtatttctta tataggccca 360  
tttaagttga aaacaatctt caaaagtccc acatcgctta gataagaaaa cgaagctgag 420  
tttatataca gctagagtcg aagtagtgat tgtcccttcg gggacatccg atcgtttttt 480  
ttctcgag 488

<210> 7  
<211> 405  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sequence of the promoter of the U3 snRNA of rice (Oryza sativa

Indica IR36)

<220>  
 <221> misc\_feature  
 <222> (1)..(6)  
 <223> EcoRI restriction site

<220>  
 <221> misc\_feature  
 <222> (7)..(384)  
 <223> Pol III promoter region

<220>  
 <221> misc\_feature  
 <222> (385)..(390)  
 <223> PvuI restriction site

<220>  
 <221> misc\_feature  
 <222> (391)..(399)  
 <223> poly T stretch

<220>  
 <221> misc\_feature  
 <222> (400)..(405)  
 <223> EcoRI restriction site

<400> 7  
 gaattcaagg gatctttaaa catacgaaca gataccttaa agttcttctg aagcaactta 60  
 aagttatcag gcatgcatgg atcttgagg aatcagatgt gcagtcaggg accatagcac 120  
 aggacaggcg tcttctactg gtgctaccag caaatgctgg aagccgggaa cactgggtac 180  
 gttggaaacc acgtgatgtg gagtaagata aactgtagga gaaaagcatt tcgtagtggg 240  
 ccatgaagcc tttcaggaca tgtattgcag tatgggccgg ccattacgc aattggacga 300  
 caacaaagac tagtattagt accacctcgg ctatccacat agatcaaagc tggtttaaaa 360  
 gagttgtgca gatgatccgt ggcacgatcg tttttttttg aattc 405

<210> 8  
 <211> 442  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> sequence of the promoter of the U3 snRNA of tomato (a garden variety with small gourd-shaped yellow fruit)

<220>  
 <221> misc\_feature  
 <222> (1)..(6)  
 <223> EcoRI restriction site

<220>  
 <221> misc\_feature  
 <222> (7)..(421)  
 <223> Pol III promoter region

<220>  
 <221> misc\_feature  
 <222> (422)..(427)  
 <223> PvuI restriction site

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<220>
<221> misc_feature
<222> (428)..(436)
<223> Poly T stretch

<220>
<221> misc_feature
<222> (437)..(442)
<223> EcoRI restriction site

<400> 8
gaattctgag agcatttgtt ggcgttcctc tgaattactt actgtcactt tgattggagc      60
cattattttc agactctact gaagattgaa ttgaatgaga aactatgaaa ctttacaagt      120
gaattattat ggagttcatg gcaactgcta tggagttttt cctactggga attggaacgg      180
tttctacgaa attaactgtc cacacgttaa aaatataaat taatgcgtaa ttgttatttt      240
ttctataaca aataaaaaac tgaaatacga cataaatttt attactttaa ttgcacttta      300
gccttagaga tattgcgttg tagtcggcgt aggtgtgtca ggggcccaata tattgttccc      360
acatcggcag tgcagcacat aaactctagc gttataagaa tctatccact atcaacggtc      420
acgatcgttt ttttttgaat tc                                              442

<210> 9
<211> 295
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<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 94bp for silencing
expression of the GUS gene (GUShp94)

<220>
<221> misc_feature
<222> (1)..(6)
<223> SalI restriction site

<220>
<221> misc_feature
<222> (6)..(11)
<223> PvuI restriction site

<220>
<221> misc_feature
<222> (12)..(100)
<223> GUS sequence (sense)

<220>
<221> misc_feature
<222> (101)..(195)
<223> spacer sequence

<220>
<221> misc_feature
<222> (190)..(195)
<223> BamHI restriction site

<220>
<221> misc_feature
<222> (196)..(284)
<223> GUS sequence (antisense)

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<220>
<221> misc_feature
<222> (285)..(290)
<223> PvuI restriction site

<220>
<221> misc_feature
<222> (290)..(295)
<223> SalI restriction site

<400> 9
gtcgacgatc gcagcgtaat gctctacacc acgccgaaca cctgggtgga cgatatcacc      60
gtggtgacgc atgtcgcgca agactgtaac cacgcgtctg ttgactggca ggtggtggcc      120
aatggtgatg tcagcgttga actgcgtgat gcggatcaac aggtggttgc aactggacaa      180
ggcactagcg ggatccagac gcgtgggttac agtcttgccg gacatgcgtc accacgggtga      240
tatcgtccac ccaggtgttc ggcgtggtgt agagcattac gctgcgatcg tcgac          295

<210> 10
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence of the dsRNA encoding region of 41 bp for silencing
expression of the GUS gene (GUShp41)

<220>
<221> misc_feature
<222> (1)..(6)
<223> SalI restriction site

<220>
<221> misc_feature
<222> (7)..(42)
<223> GUS sequence (sense)

<220>
<221> misc_feature
<222> (43)..(51)
<223> spacer sequence

<220>
<221> misc_feature
<222> (52)..(87)
<223> GUS sequence (antisense)

<220>
<221> misc_feature
<222> (88)..(93)
<223> Sal I restriction site

<400> 10
gtcgactggg cagatgaaca tggcatcgtg gtgattgatg aatgcgagaa cttcatcaat      60
caccacgatg ccatgttcat ctgcccagtc gac          93

<210> 11
<211> 50
<212> DNA
<213> Artificial Sequence

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<220>  
 <223> sequence of the dsRNA encoding region of 21 bp for silencing  
 expression of the GUS gene (GUShp21)

<220>  
 <221> misc\_feature  
 <222> (1)..(6)  
 <223> SalI restriction site

<220>  
 <221> misc\_feature  
 <222> (7)..(22)  
 <223> GUS sequence (sense)

<220>  
 <221> misc\_feature  
 <222> (23)..(28)  
 <223> spacer sequence

<220>  
 <221> misc\_feature  
 <222> (29)..(44)  
 <223> GUS sequence (antisense)

<220>  
 <221> misc\_feature  
 <222> (45)..(50)  
 <223> Sal I restriction site

<400> 11  
 gtcgactggg cagatgaaca tgtacgatca tggtcatctg cccagtcgac 50

<210> 12  
 <211> 94  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> sequence of the dsRNA encoding region of 42 bp for silencing  
 expression of the PHYB gene, derived from the 5' end of PHYB  
 (PHYB5hp42)-upper strand

<400> 12  
 tcgacggagt cgggggtagt ggcggtggcc gtggcggtgg ccgtggagga ggccacggcc 60  
 accgccacgg ccaccgccac taccctcgac tccg 94

<210> 13  
 <211> 94  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> sequence of the dsRNA encoding region of 42 bp for silencing  
 expression of the PHYB gene, derived from the 5' end of PHYB  
 (PHYB5hp42)-lower strand

<400> 13  
 tcgacggagt cgggggtagt ggcggtggcc gtggcggtgg ccgtggcctc ctccacggcc 60  
 accgccacgg ccaccgccac taccctcgac tccg 94

<210> 14

<211> 52  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> sequence of the dsRNA encoding region of 21 bp for silencing  
 expression of the PHYB gene, derived from the 5' end of PHYB  
 (PHYB5hp21)-upper strand  
  
 <400> 14  
 tcgacggagt cgggggtagt ggcggaggag gccgccacta ccccgactc cg 52  
  
 <210> 15  
 <211> 52  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> sequence of the dsRNA encoding region of 21 bp for silencing  
 expression of the PHYB gene, derived from the 5' end of PHYB  
 (PHYB5hp21)-lower strand  
  
 <400> 15  
 tcgacggagt cgggggtagt ggcggcctcc tccgccacta ccccgactc cg 52  
  
 <210> 16  
 <211> 94  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> sequence of the dsRNA encoding region of 42 bp for silencing  
 expression of the PHYB gene, derived from the center of PHYB  
 (PHYBChp42)-upper strand  
  
 <400> 16  
 tcgatggatg gtgtggttca gccatgtagg gatatggcgg gggaacagga gggttcccc 60  
 gccatatccc tacatggctg aaccacacca tcca 94  
  
 <210> 17  
 <211> 94  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> sequence of the dsRNA encoding region of 42 bp for silencing  
 expression of the PHYB gene, derived from the center of PHYB  
 (PHYBChp42)-lower strand  
  
 <400> 17  
 tcgatggatg gtgtggttca gccatgtagg gatatggcgg gggaaccctc ctgttcccc 60  
 gccatatccc tacatggctg aaccacacca tcca 94  
  
 <210> 18  
 <211> 52  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> sequence of the dsRNA encoding region of 21 bp for silencing  
 expression of the PHYB gene, derived from the center of PHYB  
 (PHYBChp21)-upper strand

<400> 18  
tcgatggatg gtgtggttca gccataggag gatggctgaa ccacacctcc aa 52

<210> 19  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sequence of the dsRNA encoding region of 21 bp for silencing  
expression of the PHYB gene, derived from the center of PHYB  
(PHYBChp21)-lower strand

<400> 19  
tcgatggatg gtgtggttca gccatcctcc tatggctgaa ccacaccatc ca 52

<210> 20  
<211> 94  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sequence of the dsRNA encoding region of 42 bp for silencing  
expression of the PHYB gene, derived from the 3' end of PHYB  
(PHYB3hp42)-upper strand

<400> 20  
tcgacattgt caactgctag tggaagtggg gacatgatgc tgatgaagga ggatcatcagc 60  
atcatgtcac cacttccact agcagttgac aatg 94

<210> 21  
<211> 94  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sequence of the dsRNA encoding region of 42 bp for silencing  
expression of the PHYB gene, derived from the 3' end of PHYB  
(PHYB3hp42)-lower strand

<400> 21  
tcgacattgt caactgctag tggaagtggg gacatgatgc tgatgacctc cttcatcagc 60  
atcatgtcac cacttccact agcagttgac aatg 94

<210> 22  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sequence of the dsRNA encoding region of 21 bp for silencing  
expression of the PHYB gene, derived from the 3' end of PHYB  
(PHYB3hp21)-upper strand

<400> 22  
tcgacattgt caactgctag tggaaaggag gttccactag cagttgacaa tg 52

<210> 23  
<211> 52  
<212> DNA

<213> Artificial Sequence

<220>  
<223> sequence of the dsRNA encoding region of 21 bp for silencing expression of the PHYB gene, derived from the 3' end of PHYB (PHYB3hp21)-lower strand

<400> 23  
tcgacattgt caactgctag tggaacctcc tttccactag cagttgacaa tg 52

<210> 24  
<211> 94  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sequence of the dsRNA encoding region of 42 bp for silencing expression of the PDS gene (PDS42)-upper strand

<400> 24  
tcgacttaac ttgtaaggaa tattacgatc ctaaccggtc aatgctagga ggagcattga 60  
ccggttagga tcgtaatatt ccttacaagt taag 94

<210> 25  
<211> 94  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sequence of the dsRNA encoding region of 42 bp for silencing expression of the PDS gene (PDS42)-lower strand

<400> 25  
tcgacttaac ttgtaaggaa tattacgatc ctaaccggtc aatgctcctc ctagcattga 60  
ccggttagga tcgtaatatt ccttacaagt taag 94

<210> 26  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sequence of the dsRNA encoding region of 21 bp for silencing expression of the PDS gene (PDS21)-upper strand

<400> 26  
tcgacttaac ttgtaaggaa tattaaggag gtaatattcc ttacaagtta ag 52

<210> 27  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sequence of the dsRNA encoding region of 21 bp for silencing expression of the PDS gene (PDS21)-lower strand

<400> 27  
tcgacttaac ttgtaaggaa tattacctcc ttaatattcc ttacaagtta ag 52

<210> 28

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<211> 115
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<213> Artificial sequence

<220>
<223> small hairpin RNA coding region (GUS_A)

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<222> (1)..(11)
<223> SalI/PvuI restriction sites

<220>
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<222> (12)..(53)
<223> sense RNA encoding region

<220>
<221> misc_feature
<222> (54)..(62)
<223> loop structure

<220>
<221> misc_feature
<222> (63)..(104)
<223> antisense RNA encoding region

<220>
<221> misc_feature
<222> (105)..(115)
<223> SalI/PvuI restriction sites

<400> 28
gtcgacgatc gtgcggtcac tcattacggc aaagtgtggg tcaataatca ggagttcctt 60
cttcctgatt attgaccac actttgccgt aatgagtgac cgcagtcgac gatcg 115

<210> 29
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<212> DNA
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<220>
<223> small hairpin RNA coding region (GUS_B)

<220>
<221> misc_feature
<222> (1)..(8)
<223> SalI/PvuI restriction sites

<220>
<221> misc_feature
<222> (9)..(50)
<223> sense RNA encoding sequence

<220>
<221> misc_feature
<222> (51)..(59)
<223> loop structure

<220>
<221> misc_feature
<222> (60)..(101)
<223> antisense RNA coding region

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<220>
<221> misc_feature
<222> (102)..(112)
<223> SalI/pvuI restriction site

<400> 29
gtcgacgatc gtcatgaaga tgcggacttg cgtggcaaag gattcgataa gttccttctt      60
tatcgaatcc tttgccacgc aagtccgcat cttcatgacg agtcgacgat cg                112

<210> 30
<211> 115
<212> DNA
<213> Artificial sequence

<220>
<223> small hairpin RNA coding region (GUS_C)

<220>
<221> misc_feature
<222> (1)..(11)
<223> SalI/PvuI restriction sites

<220>
<221> misc_feature
<222> (12)..(53)
<223> sense RNA coding region

<220>
<221> misc_feature
<222> (54)..(62)
<223> loop structure

<220>
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